PCT

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                 RAW SEQUENCE LISTING          DATE: 12/26/2000
                 PATENT APPLICATION:  US/09/673,198    TIME: 13:19:35

                 Input Set : A:\1241.16 sequence.txt
                 Output Set: N:\CRF3\12262000\I673198.raw
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     2 <110> APPLICANT: MIYAKE, Koichiro; HASHIMOTO, Shinichi; MOTOYAMA Hiroaki;
     3         OZAKI, Akio; SETO, Haruo; KUZAYAMA, Tomohisa; TAKAHASHI, Shunji
     5 <120> TITLE OF INVENTION: A process for producing isoprenoid compounds by
     6         microorganisms and a method for screening compounds with
     7         antibiotic or weeding activity
W--> 9 <130> FILE REFERENCE:
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/673,198
C--> 12 <141> CURRENT FILING DATE: 2000-10-12
    14 <150> PRIOR APPLICATION NUMBER: JP98/103101
    15 <151> PRIOR FILING DATE: 1998-04-14
    17 <150> PRIOR APPLICATION NUMBER: JP98/221910
    18 <151> PRIOR FILING DATE: 1998-08-05
    20 <150> PRIOR APPLICATION NUMBER: JP99/035739
    21 <151> PRIOR FILING DATE: 1999-02-15
    23 <160> NUMBER OF SEQ ID NOS: 34
    25 <170> SOFTWARE: PatentIn Ver. 2.0


ERRORED SEQUENCES

   392 <210> SEQ ID NO: 6
   393 <211> LENGTH: 1860
   394 <212> TYPE: DNA
   395 <213> ORGANISM: Escherichia coli
   397 <220> FEATURE:
   398 <221> NAME/KEY: CDS
   399 <222> LOCATION: (1)..(1860)
   401 <400> SEQUENCE: 6
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   403 48
   405 Met Ser Phe Asp Ile Ala Lys Tyr Pro Thr Leu Ala Leu Val Asp Ser
   406  1               5                   10                  15
E--> 408 acc cag gag tta cga ctg ttg ccg aaa gag agt tta ccg aaa ctc tgc
   409 96
   411 Thr Gln Glu Leu Arg Leu Leu Pro Lys Glu Ser Leu Pro Lys Leu Cys
   412              20                  25                  30
E--> 414 gac gaa ctg cgc cgc tat tta ctc gac agc gtg agc cgt tcc agc ggg
   415 144
   417 Asp Glu Leu Arg Arg Tyr Leu Leu Asp Ser Val Ser Arg Ser Ser Gly
   418              35                  40                  45
E--> 420 cac ttc gcc tcc ggg ctg ggc acg gtc gaa ctg acc gtg gcg ctg cac
   421 192
   423 His Phe Ala Ser Gly Leu Gly Thr Val Glu Leu Thr Val Ala Leu His
   424      50                  55                  60
E--> 426 tat gtc tac aac acc ccg ttt gac caa ttg att tgg gat gtg ggg cat
   427 240
   429 Tyr Val Tyr Asn Thr Pro Phe Asp Gln Leu Ile Trp Asp Val Gly His
```

formatena
48

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     430  65                    70                   75                    80
E--> 432 cag gct tat ccg cat aaa att ttg acc gga cgc cgc gac aaa atc ggc
     433 288
     435 Gln Ala Tyr Pro His Lys Ile Leu Thr Gly Arg Arg Asp Lys Ile Gly
     436                85                   90                   95
E--> 438 acc atc cgt cag aaa ggc ggt ctg cac ccg ttc ccg tgg cgc ggc gaa
     439 336
     441 Thr Ile Arg Gln Lys Gly Gly Leu His Pro Phe Pro Trp Arg Gly Glu
     442                100                  105                  110
E--> 444 agc gaa tat gac gta tta agc gtc ggg cat tca tca acc tcc atc agt
     445 384
     447 Ser Glu Tyr Asp Val Leu Ser Val Gly His Ser Ser Thr Ser Ile Ser
     448                115                  120                  125
E--> 450 gcc gga att ggt att gcg gtt gct gcc gaa aaa gaa ggc aaa aat cgc
     451 432
     453 Ala Gly Ile Gly Ile Ala Val Ala Ala Glu Lys Glu Gly Lys Asn Arg
     454       130                  135                  140
E--> 456 cgc acc gtc tgt gtc att ggc gat ggc gcg att acc gca ggc atg gcg
     457 480
     459 Arg Thr Val Cys Val Ile Gly Asp Gly Ala Ile Thr Ala Gly Met Ala
     460 145                  150                  155                  160
E--> 462 ttt gaa gcg atg aat cac gcg ggc gat atc cgt cct gat atg ctg gtg
     463 528
     465 Phe Glu Ala Met Asn His Ala Gly Asp Ile Arg Pro Asp Met Leu Val
     466                165                  170                  175
E--> 468 att ctc aac gac aat gaa atg tcg att tcc gaa aat gtc ggc gcg ctc
     469 576
     471 Ile Leu Asn Asp Asn Glu Met Ser Ile Ser Glu Asn Val Gly Ala Leu
     472                180                  185                  190
E--> 474 aac aac cat ctg gca cag ctg ctt tcc ggt aag ctt tac tct tca ctg
     475 624
     477 Asn Asn His Leu Ala Gln Leu Leu Ser Gly Lys Leu Tyr Ser Ser Leu
     478                195                  200                  205
E--> 480 cgc gaa ggc ggg aaa aaa gtt ttc tct ggc gtg ccg cca att aaa gag
     481 672
     483 Arg Glu Gly Gly Lys Lys Val Phe Ser Gly Val Pro Pro Ile Lys Glu
     484       210                  215                  220
E--> 486 ctg ctc aaa cgc acc gaa gaa cat att aaa ggc atg gta gtg cct ggc
     487 720
     489 Leu Leu Lys Arg Thr Glu Glu His Ile Lys Gly Met Val Val Pro Gly
     490 225                  230                  235                  240
E--> 492 acg ttg ttt gaa gag ctg ggc ttt aac tac atc ggc ccg gtg gac ggt
     493 768
     495 Thr Leu Phe Glu Glu Leu Gly Phe Asn Tyr Ile Gly Pro Val Asp Gly
     496                245                  250                  255
E--> 498 cac gat gtg ctg ggg ctt atc acc acg cta aag aac atg cgc gac ctg
     499 816
     501 His Asp Val Leu Gly Leu Ile Thr Thr Leu Lys Asn Met Arg Asp Leu
     502                260                  265                  270
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E--> 504 aaa ggc ccg cag ttc ctg cat atc atg acc aaa aaa ggt cgt ggt tat
     505 864
     507 Lys Gly Pro Gln Phe Leu His Ile Met Thr Lys Lys Gly Arg Gly Tyr
     508         275                 280                 285
E--> 510 gaa ccg gca gaa aaa gac ccg atc act ttc cac gcc gtg cct aaa ttt
     511 912
     513 Glu Pro Ala Glu Lys Asp Pro Ile Thr Phe His Ala Val Pro Lys Phe
     514         290                 295                 300  .
E--> 516 gat ccc tcc agc ggt tgt ttg ccg aaa agt agc ggc ggt ttg ccg agc
     517 960
     519 Asp Pro Ser Ser Gly Cys Leu Pro Lys Ser Ser Gly Gly Leu Pro Ser
     520 305                 310                 315                 320
E--> 522 tat tca aaa atc ttt ggc gac tgg ttg tgc gaa acg gca gcg aaa gac
     523 1008
     525 Tyr Ser Lys Ile Phe Gly Asp Trp Leu Cys Glu Thr Ala Ala Lys Asp
     526             325                 330                 335
E--> 528 aac aag ctg atg gcg att act ccg gcg atg cgt gaa ggt tcc ggc atg
     529 1056
     531 Asn Lys Leu Met Ala Ile Thr Pro Ala Met Arg Glu Gly Ser Gly Met
     532         340                 345                 350
E--> 534 gtc gag ttt tca cgt aaa ttc ccg gat cgc tac ttc gac gtg gca att
     535 1104
     537 Val Glu Phe Ser Arg Lys Phe Pro Asp Arg Tyr Phe Asp Val Ala Ile
     538         355                 360                 365
E--> 540 gcc gag caa cac gcg gtg acc ttt gct gcg ggt ctg gcg att ggt ggg
     541 1152
     543 Ala Glu Gln His Ala Val Thr Phe Ala Ala Gly Leu Ala Ile Gly Gly
     544         370                 375                 380
E--> 546 tac aaa ccc att gtc gcg att tac tcc act ttc ctg caa cgc gcc tat
     547 1200
     549 Tyr Lys Pro Ile Val Ala Ile Tyr Ser Thr Phe Leu Gln Arg Ala Tyr
     550 385                 390                 395                 400
E--> 552 gat cag gtg ctg cat gac gtg gcg att caa aag ctt ccg gtc ctg ttc
     553 1248
     555 Asp Gln Val Leu His Asp Val Ala Ile Gln Lys Leu Pro Val Leu Phe
     556             405                 410                 415
E-->'558 gcc atc gac cgc gcg ggc att gtt ggt gct gac ggt caa acc cat cag
     559 1296
     561 Ala Ile Asp Arg Ala Gly Ile Val Gly Ala Asp Gly Gln Thr His Gln
     562         420                 425                 430
E--> 564 ggt gct ttt gat ctc tct tac ctg cgc tgc ata ccg gaa atg gtc att
     565 1344
     567 Gly Ala Phe Asp Leu Ser Tyr Leu Arg Cys Ile Pro Glu Met Val Ile
     568         435                 440                 445
E--> 570 atg acc ccg agc gat gaa aac gaa tgt cgc cag atg ctc tat acc ggc
    .571 1392
     573 Met Thr Pro Ser Asp Glu Asn Glu Cys Arg Gln Met Leu Tyr Thr Gly
     574     450  .             455                 460
E--> 576 tat cac tat aac gat ggc ccg tca gcg gtg cgc tac ccg cgt ggc aac
```

```
            RAW SEQUENCE LISTING              DATE: 12/26/2000
            PATENT APPLICATION:  US/09/673,198    TIME: 13:19:35

            Input Set : A:\1241.16 sequence.txt
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        577 1440
        579 Tyr His Tyr Asn Asp Gly Pro Ser Ala Val Arg Tyr Pro Arg Gly Asn
        580 465             470             475             480
E-->    582 gcg gtc ggc gtg gaa ctg acg ccg ctg gaa aaa cta cca att ggc aaa
        583 1488
        585 Ala Val Gly Val Glu Leu Thr Pro Leu Glu Lys Leu Pro Ile Gly Lys
        586             485             490             495
E-->    588 ggc att gtg aag cgt cgt ggc gag aaa ctg gcg atc ctt aac ttt ggt
        589 1536
        591 Gly Ile Val Lys Arg Arg Gly Glu Lys Leu Ala Ile Leu Asn Phe Gly
        592             500             505             510
E-->    594 acg ctg atg cca gaa gcg gcg aaa gtc gcc gaa tcg ctg aac gcc acg
        595 1584
        597 Thr Leu Met Pro Glu Ala Ala Lys Val Ala Glu Ser Leu Asn Ala Thr
        598             515             520             525
E-->    600 ctg gtc gat atg cgt ttt gtg aaa ccg ctt gat gaa gcg tta att ctg
        601 1632
        603 Leu Val Asp Met Arg Phe Val Lys Pro Leu Asp Glu Ala Leu Ile Leu
        604         530             535             540
E-->    606 gaa atg gcc gcc agc cat gaa gcg ctg gtc acc gta gaa gaa aac gcc
        607 1680
        609 Glu Met Ala Ala Ser His Glu Ala Leu Val Thr Val Glu Glu Asn Ala
        610 545             550             555             560
E-->    612 att atg ggc ggc gca ggc agc ggc gtg aac gaa gtg ctg atg gcc cat
        613 1728
        615 Ile Met Gly Gly Ala Gly Ser Gly Val Asn Glu Val Leu Met Ala His
        616             565             570             575
E-->    618 cgt aaa cca gta ccc gtg ctg aac att ggc ctg ccg gac ttc ttt att
        619 1776
        621 Arg Lys Pro Val Pro Val Leu Asn Ile Gly Leu Pro Asp Phe Phe Ile
        622             580             585             590
E-->    624 ccg caa gga act cag gaa gaa atg cgc gcc gaa ctc ggc ctc gat gcc
        625 1824
        627 Pro Gln Gly Thr Gln Glu Glu Met Arg Ala Glu Leu Gly Leu Asp Ala
        628             595             600             605
E-->    630 gct ggt atg gaa gcc aaa atc aag gcc tgg ctg gca
        631 1860
        633 Ala Gly Met Glu Ala Lys Ile Lys Ala Trp Leu Ala
        634         610             615             620
        637 <210> SEQ ID NO: 7
        638 <211> LENGTH: 897
        639 <212> TYPE: DNA
        640 <213> ORGANISM: Escherichia coli
        642 <220> FEATURE:
        643 <221> NAME/KEY: CDS
        644 <222> LOCATION: (1)..(897)
        646 <400> SEQUENCE: 7
E-->    647 atg gac ttt ccg cag caa ctc gaa gcc tgc gtt aag cag gcc aac cag
        648 48
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       650 Met Asp Phe Pro Gln Gln Leu Glu Ala Cys Val Lys Gln Ala Asn Gln
       651   1                 5                 10                15
E--> 653 gcg ctg agc cgt ttt atc gcc cca ctg ccc ttt cag aac act ccc gtg
       654 96
       656 Ala Leu Ser Arg Phe Ile Ala Pro Leu Pro Phe Gln Asn Thr Pro Val
       657               20                 25                 30
E--> 659 gtc gaa acc atg cag tat ggc gca tta tta ggt ggt aag cgc ctg cga
       660 144
       662 Val Glu Thr Met Gln Tyr Gly Ala Leu Leu Gly Gly Lys Arg Leu Arg
       663               35                 40                 45
E--> 665 cct ttc ctg gtt tat gcc acc ggt cat atg ttc ggc gtt agc aca aac
       666 192
       668 Pro Phe Leu Val Tyr Ala Thr Gly His Met Phe Gly Val Ser Thr Asn
       669         50                 55                 60
E--> 671 acg ctg gac gca ccc gct gcc gcc gtt gag tgt atc cac gct tac tca
       672 240
       674 Thr Leu Asp Ala Pro Ala Ala Ala Val Glu Cys Ile His Ala Tyr Ser
       675 65                 70                 75                 80
E--> 677 tta att cat gat gat tta ccg gca atg gat gat gac gat ctg cgt cgc
       678 288
       680 Leu Ile His Asp Asp Leu Pro Ala Met Asp Asp Asp Leu Arg Arg
       681                 85                 90                 95
E--> 683 ggt ttg cca acc tgc cat gtg aag ttt ggc gaa gca aac gcg att ctc
       684 336
       686 Gly Leu Pro Thr Cys His Val Lys Phe Gly Glu Ala Asn Ala Ile Leu
       687               100                105                110
E--> 689 gct ggc gac gct tta caa acg ctg gcg ttc tcg att tta agc gat gcc
       690 384
       692 Ala Gly Asp Ala Leu Gln Thr Leu Ala Phe Ser Ile Leu Ser Asp Ala
       693               115                120                125
E--> 695 gat atg ccg gaa gtg tcg gac cgc gac aga att tcg atg att tct gaa
       696 432
       698 Asp Met Pro Glu Val Ser Asp Arg Asp Arg Ile Ser Met Ile Ser Glu
       699   . 130                135                140
E--> 701 ctg gcg agc gcc agt ggt att gcc gga atg tgc ggt ggt cag gca tta
       702 480
       704 Leu Ala Ser Ala Ser Gly Ile Ala Gly Met Cys Gly Gly Gln Ala Leu
       705 145                150                155                160
E--> 707 gat tta gac gcg gaa ggc aaa cac gta cct ctg gac gcg ctt gag cgt
       708 528
       710 Asp Leu Asp Ala Glu Gly Lys His Val Pro Leu Asp Ala Leu Glu Arg
       711               165                170                175
E--> 713 att cat cgt cat aaa acc ggc gca ttg att cgc gcc gcc gtt cgc ctt
       714 576
       716 Ile His Arg His Lys Thr Gly Ala Leu Ile Arg Ala Ala Val Arg Leu
       717               180                185                190
E--> 719 ggt gca tta agc gcc gga gat aaa gga cgt cgt gct ctg ccg gta ctc
       720 624
       722 Gly Ala Leu Ser Ala Gly Asp Lys Gly Arg Arg Ala Leu Pro Val Leu
```

```
       723          195                   200                 205
E--> 725 gac aag tat gca gag agc atc ggc ctt gcc ttc cag gtt cag gat gac
     726 672
     728 Asp Lys Tyr Ala Glu Ser Ile Gly Leu Ala Phe Gln Val Gln Asp Asp
     729      210               215               220
E--> 731 atc ctg gat gtg gtg gga gat act gca acg ttg gga aaa cgc cag ggt
     732 720
     734 Ile Leu Asp Val Val Gly Asp Thr Ala Thr Leu Gly Lys Arg Gln Gly
     735 225               230               235                    240
E--> 737 gcc gac cag caa ctt ggt aaa agt acc tac cct gca ctt ctg ggt ctt
     738 768
     740 Ala Asp Gln Gln Leu Gly Lys Ser Thr Tyr Pro Ala Leu Leu Gly Leu
     741               245               250                    255
E--> 743 gag caa gcc cgg aag aaa gcc cgg gat ctg atc gac gat gcc cgt cag
     744 816
     746 Glu Gln Ala Arg Lys Lys Ala Arg Asp Leu Ile Asp Asp Ala Arg Gln
     747               260               265               270
E--> 749 tcg ctg aaa caa ctg gct gaa cag tca ctc gat acc tcg gca ctg gaa
     750 864
     752 Ser Leu Lys Gln Leu Ala Glu Gln Ser Leu Asp Thr Ser Ala Leu Glu
     753          275                   280                 285
E--> 755 gcg cta gcg gac tac atc atc cag cgt aat aaa
     756 897
     758 Ala Leu Ala Asp Tyr Ile Ile Gln Arg Asn Lys
     759      290               295
     762 <210> SEQ ID NO: 8
     763 <211> LENGTH: 240
     764 <212> TYPE: DNA
     765 <213> ORGANISM: Escherichia coli
     767 <220> FEATURE:
     768 <221> NAME/KEY: CDS
     769 <222> LOCATION: (1)..(240)
     771 <400> SEQUENCE: 8
E--> 772 atg ccg aag aaa aat gag gcg ccc gcc agc ttt gaa aag gcg ctg agc
     773 48
     775 Met Pro Lys Lys Asn Glu Ala Pro Ala Ser Phe Glu Lys Ala Leu Ser
     776   1               5                   10                  15
E--> 778 gag ctg gaa cag att gta acc cgt ctg gaa agt ggc gac ctg ccg ctg
     779 96
     781 Glu Leu Glu Gln Ile Val Thr Arg Leu Glu Ser Gly Asp Leu Pro Leu
     782               20                  25                  30
E--> 784 gaa gag gcg ctg aac gag ttc gaa cgc ggc gtg cag ctg gca cgt cag
     785 144
     787 Glu Glu Ala Leu Asn Glu Phe Glu Arg Gly Val Gln Leu Ala Arg Gln
     788               35                  40                  45
E--> 790 ggg cag gcc aaa tta caa caa gcc gaa cag cgc gta caa att ctg ctg
     791 192
     793 Gly Gln Ala Lys Leu Gln Gln Ala Glu Gln Arg Val Gln Ile Leu Leu
     794      50               55               60
```

```
E--> 796 tct gac aat gaa gac gcc tct cta acc cct ttt aca ccg gac aat gag
    797 240
        799 Ser Asp Asn Glu Asp Ala Ser Leu Thr Pro Phe Thr Pro Asp Asn Glu
        800  65                  70              75          Pro          80
    803 <210> SEQ ID NO: 9
    804 <211> LENGTH: 1044
    805 <212> TYPE: DNA
    806 <213> ORGANISM: Escherichia coli
    808 <220> FEATURE:
    809 <221> NAME/KEY: CDS
    810 <222> LOCATION: (1)..(1044)
    812 <400> SEQUENCE: 9
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    814 48
        816 Val Thr Gly Val Asn Glu Cys Ser Arg Ser Thr Cys Asn Leu Lys Tyr
        817  1                   5              10              15
E--> 819 gac gag tat agc agg agt ggc agc atg caa tac aac ccc tta gga aaa
    820 96
        822 Asp Glu Tyr Ser Arg Ser Gly Ser Met Gln Tyr Asn Pro Leu Gly Lys
        823             20              25              30
E--> 825 acc gac ctt cgc gtt tcc cga ctt tgc ctc ggc tgt atg acc ttt ggc
    826 144
        828 Thr Asp Leu Arg Val Ser Arg Leu Cys Leu Gly Cys Met Thr Phe Gly
        829         35              40              45
E--> 831 gag cca gat cgc ggt aat cac gca tgg aca ctg ccg gaa gaa agc agc
    832 192
        834 Glu Pro Asp Arg Gly Asn His Ala Trp Thr Leu Pro Glu Glu Ser Ser
        835         50              55              60
E--> 837 cgt ccc ata att aaa cgt gca ctg gaa ggc ggc ata aat ttc ttt gat
    838 240
        840 Arg Pro Ile Ile Lys Arg Ala Leu Glu Gly Gly Ile Asn Phe Phe Asp
        841  65                  70              75                  80
E--> 843 acc gcc aac agt tat tct gac ggc agc agc gaa gag atc gtc ggt cgc
    844 288
        846 Thr Ala Asn Ser Tyr Ser Asp Gly Ser Ser Glu Glu Ile Val Gly Arg
        847             85              90                  95
E--> 849 gca ctg cgg gat ttc gcc cgt cgt gaa gac gtg gtc gtt gcg acc aaa
    850 336
        852 Ala Leu Arg Asp Phe Ala Arg Arg Glu Asp Val Val Val Ala Thr Lys
        853         100             105             110
E--> 855 gtg ttc cat cgc gtt ggt gat tta ccg gaa gga tta tcc cgt gcg caa
    856 384
        858 Val Phe His Arg Val Gly Asp Leu Pro Glu Gly Leu Ser Arg Ala Gln
        859         115             120             125
E--> 861 att ttg cgc tct atc gac gac agc ctg cga cgt ctc ggc atg gat tat
    862 432
        864 Ile Leu Arg Ser Ile Asp Asp Ser Leu Arg Arg Leu Gly Met Asp Tyr
        865         130             135             140
E--> 867 gtc gat atc ctg caa att cat cgc tgg gat tac aac acg ccg atc gaa
```

```
        868 480
        870 Val Asp Ile Leu Gln Ile His Arg Trp Asp Tyr Asn Thr Pro Ile Glu
        871 145               150               155               160
E--> 873 gag acg ctg gaa gcc ctc aac gac gtg gta aaa gcc ggg aaa gcg cgt
        874 528
        876 Glu Thr Leu Glu Ala Leu Asn Asp Val Val Lys Ala Gly Lys Ala Arg
        877             165               170               175
E--> 879 tat atc ggc gcg tca tca atg cac gct tcg cag ttt gct cag gca ctg
        880 576
        882 Tyr Ile Gly Ala Ser Ser Met His Ala Ser Gln Phe Ala Gln Ala Leu
        883             180               185               190
E--> 885 gaa ctc caa aaa cag cac ggc tgg gcg cag ttt gtc agt atg cag gat
        886 624
        888 Glu Leu Gln Lys Gln His Gly Trp Ala Gln Phe Val Ser Met Gln Asp
        889         195               200               205
E--> 891 cac tac aat ctg att tat cgt gaa gaa gag cgc gag atg cta cca ctg
        892 672
        894 His Tyr Asn Leu Ile Tyr Arg Glu Glu Glu Arg Glu Met Leu Pro Leu
        895     210               215               220
E--> 897 tgt tat cag gag ggc gtg gcg gta att cca tgg agc ccg ctg gca agg
        898 720
        900 Cys Tyr Gln Glu Gly Val Ala Val Ile Pro Trp Ser Pro Leu Ala Arg
        901 225               230               235               240
E--> 903 ggc cgt ctg acg cgt ccg tgg gga gaa act acc gca cga ctg gtg tct
        904 768
        906 Gly Arg Leu Thr Arg Pro Trp Gly Glu Thr Thr Ala Arg Leu Val Ser
        907             245               250               255
E--> 909 gat gag gtg ggg aaa aat ctc tat aaa gaa agc gat gaa aat gac gcg
        910 816
        912 Asp Glu Val Gly Lys Asn Leu Tyr Lys Glu Ser Asp Glu Asn Asp Ala
        913             260               265               270
E--> 915 cag atc gca gag cgg tta aca ggc gtc agt gaa gaa ctg ggg gcg aca
        916 864
        918 Gln Ile Ala Glu Arg Leu Thr Gly Val Ser Glu Glu Leu Gly Ala Thr
        919         275               280               285
E--> 921 cga gca caa gtt gcg ctg gcc tgg ttg ttg agt aaa ccg ggc att gcc
        922 912
        924 Arg Ala Gln Val Ala Leu Ala Trp Leu Leu Ser Lys Pro Gly Ile Ala
        925     290               295               300
E--> 927 gca ccg att atc gga act tcg cgc gaa gaa cag ctt gat gag cta ttg
        928 960
        930 Ala Pro Ile Ile Gly Thr Ser Arg Glu Glu Gln Leu Asp Glu Leu Leu
        931 305               310               315               320
E--> 933 aac gcg gtg gat atc act ttg aag ccg gaa cag att gcc gaa ctg gaa
        934 1008
        936 Asn Ala Val Asp Ile Thr Leu Lys Pro Glu Gln Ile Ala Glu Leu Glu
        937             325               330               335
E--> 939 acg ccg tat aaa ccg cat cct gtc gta gga ttt aaa
        940 1044
```

RAW SEQUENCE LISTING   DATE: 12/26/2000
PATENT APPLICATION: US/09/673,198   TIME: 13:19:35

Input Set : A:\1241.16 sequence.txt
Output Set: N:\CRF3\12262000\I673198.raw

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        943             340                 345
        946 <210> SEQ ID NO: 10
        947 <211> LENGTH: 1194
        948 <212> TYPE: DNA
        949 <213> ORGANISM: Escherichia coli
        951 <220> FEATURE:
        952 <221> NAME/KEY: CDS
        953 <222> LOCATION: (1)..(1194)
        955 <400> SEQUENCE: 10
E--> 956 atg aag caa ctc acc att ctg ggc tcg acc ggc tcg att ggt tgc agc
     957 48
        959 Met Lys Gln Leu Thr Ile Leu Gly Ser Thr Gly Ser Ile Gly Cys Ser
        960  1               5              10                  15
E--> 962 acg ctg gac gtg gtg cgc cat aat ccc gaa cac ttc cgc gta gtt gcg
     963 96
        965 Thr Leu Asp Val Val Arg His Asn Pro Glu His Phe Arg Val Val Ala
        966             20              25                  30
E--> 968 ctg gtg gca ggc aaa aat gtc act cgc atg gta gaa cag tgc ctg gaa
     969 144
        971 Leu Val Ala Gly Lys Asn Val Thr Arg Met Val Glu Gln Cys Leu Glu
        972             35              40                  45
E--> 974 ttc tct ccc cgc tat gcc gta atg gac gat gaa gcg agt gcg aaa ctt
     975 192
        977 Phe Ser Pro Arg Tyr Ala Val Met Asp Asp Glu Ala Ser Ala Lys Leu
        978         50              55                  60
E--> 980 ctt aaa acg atg cta cag caa cag ggt agc cgc acc gaa gtc tta agt
     981 240
        983 Leu Lys Thr Met Leu Gln Gln Gln Gly Ser Arg Thr Glu Val Leu Ser
        984 65              70                  75                  80
E--> 986 ggg caa caa gcc gct tgc gat atg gca gcg ctt gag gat gtt gat cag
     987 288
        989 Gly Gln Gln Ala Ala Cys Asp Met Ala Ala Leu Glu Asp Val Asp Gln
        990             85              90                  95
E--> 992 gtg atg gca gcc att gtt ggc gct gct ggg ctg tta cct acg ctt gct
     993 336
        995 Val Met Ala Ala Ile Val Gly Ala Ala Gly Leu Leu Pro Thr Leu Ala
        996             100             105                 110
E--> 998 gcg atc cgc gcg ggt aaa acc att ttg ctg gcc aat aaa gaa tca ctg
     999 384
        1001 Ala Ile Arg Ala Gly Lys Thr Ile Leu Leu Ala Asn Lys Glu Ser Leu
        1002            115             120                 125
E--> 1004 gtt acc tgc gga cgt ctg ttt atg gac gcc gta aag cag agc aaa gcg
     1005 432
        1007 Val Thr Cys Gly Arg Leu Phe Met Asp Ala Val Lys Gln Ser Lys Ala
        1008        130             135                 140
E--> 1010 caa ttg tta ccg gtc gat agc gaa cat aac gcc att ttt cag agt tta
     1011 480
        1013 Gln Leu Leu Pro Val Asp Ser Glu His Asn Ala Ile Phe Gln Ser Leu
```

```
     1014 145                    150                 155                   160
E--> 1016 ccg caa cct atc cag cat aat ctg gga tac gct gac ctt gag caa aat
     1017 528
     1019 Pro Gln Pro Ile Gln His Asn Leu Gly Tyr Ala Asp Leu Glu Gln Asn
     1020                    165               170                   175
E--> 1022 ggc gtg gtg tcc att tta ctt acc ggg tct ggt ggc cct ttc cgt gag
     1023 576
     1025 Gly Val Val Ser Ile Leu Leu Thr Gly Ser Gly Gly Pro Phe Arg Glu
     1026                    180                 185               190
E--> 1028 acg cca ttg cgc gat ttg gca aca atg acg ccg gat caa gcc tgc cgt
     1029 624
     1031 Thr Pro Leu Arg Asp Leu Ala Thr Met Thr Pro Asp Gln Ala Cys Arg
     1032                195               200                   205
E--> 1034 cat ccg aac tgg tcg atg ggg cgt aaa att tct gtc gat tcg gct acc
     1035 672
     1037 His Pro Asn Trp Ser Met Gly Arg Lys Ile Ser Val Asp Ser Ala Thr
     1038        210                 215                 220
E--> 1040 atg atg aac aaa ggt ctg gaa tac att gaa gcg cgt tgg ctg ttt aac
     1041 720
     1043 Met Met Asn Lys Gly Leu Glu Tyr Ile Glu Ala Arg Trp Leu Phe Asn
     1044 225                    230                 235                   240
E--> 1046 gcc agc gcc agc cag atg gaa gtg ctg att cac ccg cag tca gtg att
     1047 768
     1049 Ala Ser Ala Ser Gln Met Glu Val Leu Ile His Pro Gln Ser Val Ile
     1050                    245                 250                   255
E--> 1052 cac tca atg gtg cgc tat cag gac ggc agt gtt ctg gcg cag ctg ggg
     1053 816
     1054 His Ser Met Val Arg Tyr Gln Asp Gly Ser Val Leu Ala Gln Leu Gly
     1055                260                 265                 270
E--> 1057 gaa ccg gat atg gta cgc caa ttg ccc aca cca tgg gca tgg ccg aat
     1058 864
     1060 Glu Pro Asp Met Val Arg Gln Leu Pro Thr Pro Trp Ala Trp Pro Asn
     1061        275                 280                 285
E--> 1063 cgc gtg aac tct ggc gtg aag ccg ctc gat ttt tgc aaa cta agt gcg
     1064 912
     1066 Arg Val Asn Ser Gly Val Lys Pro Leu Asp Phe Cys Lys Leu Ser Ala
     1067        290                 295                 300
E--> 1069 ttg aca ttt gcc gca ccg gat tat gat cgt tat cca tgc ctg aaa ctg
     1070 960
     1072 Leu Thr Phe Ala Ala Pro Asp Tyr Asp Arg Tyr Pro Cys Leu Lys Leu
     1073 305                    310                 315                   320
E--> 1075 gcg atg gag gcg ttc gaa caa ggc cag gca gcg acg aca gca ttg aat
     1076 1008
     1078 Ala Met Glu Ala Phe Glu Gln Gly Gln Ala Ala Thr Thr Ala Leu Asn
     1079                    325                 330                   335
E--> 1081 gcc gca aac gaa atc acc gtt gct gct ttt ctt gcg caa caa atc cgc
     1082 1056
     1084 Ala Ala Asn Glu Ile Thr Val Ala Ala Phe Leu Ala Gln Gln Ile Arg
     1085                    340                 345                   350
```

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```
E--> 1087 ttt acg gat atc gct gcg ttg aat tta tcc gta ctg gaa aaa atg gat
     1088 1104
     1090 Phe Thr Asp Ile Ala Ala Leu Asn Leu Ser Val Leu Glu Lys Met Asp
     1091          355              360              365
E--> 1093 atg cgc gaa cca caa tgt gtg gac gat gtg tta tct gtt gat gcg aac
     1094 1152
     1096 Met Arg Glu Pro Gln Cys Val Asp Asp Val Leu Ser Val Asp Ala Asn
     1097          370              375              380
E--> 1099 gcg cgt gaa gtc gcc aga aaa gag gtg atg cgt ctc gca agc
     1100 1194
     1102 Ala Arg Glu Val Ala Arg Lys Glu Val Met Arg Leu Ala Ser
     1103 385              390              395
     1106 <210> SEQ ID NO: 11
     1107 <211> LENGTH: 4390
     1108 <212> TYPE: DNA
     1109 <213> ORGANISM: Escherichia coli
     1111 <220> FEATURE:
     1112 <221> NAME/KEY: CDS
     1113 <222> LOCATION: (208)..(447)
     1115 <220> FEATURE:
     1116 <221> NAME/KEY: CDS
     1117 <222> LOCATION: (450)..(1346)
     1119 <220> FEATURE:
     1120 <221> NAME/KEY: CDS
     1121 <222> LOCATION: (1374)..(3233)
     1123 <220> FEATURE:
     1124 <221> NAME/KEY: CDS
     1125 <222> LOCATION: (3344)..(4390)
     1127 <400> SEQUENCE: 11
E--> 1128 atggcggcaa tggttcgttg gcaagcctta agcgacttgt atagggaaaa atacagcagc
     1129 60
E--> 1132 ccacacctgc ggctgcatcc aggcgcggaa gtataccact aacatcgctt tgctgtgcac
     1133 120
E--> 1136 atcaccttac cattgcgcgt tatttgctat ttgccctgag tccgttacca tgacggggcg
     1137 180
E--> 1140 aaaaatattg agagtcagac attcatt atg ccg aag aaa aat gag gcg ccc gcc
     1141 234
     1143                                    Met Pro Lys Lys Asn Glu Ala Pro Ala
     1144                                    1               5
E--> 1146 agc ttt gaa aag gcg ctg agc gag ctg gaa cag att gta acc cgt ctg
     1147 282
     1149 Ser Phe Glu Lys Ala Leu Ser Glu Leu Glu Gln Ile Val Thr Arg Leu
     1150 10              15              20              25
E--> 1152 gaa agt ggc gac ctg ccg ctg gaa gag gcg ctg aac gag ttc gaa cgc
     1153 330
     1155 Glu Ser Gly Asp Leu Pro Leu Glu Glu Ala Leu Asn Glu Phe Glu Arg
     1156          30              35              40
E--> 1158 ggc gtg cag ctg gca cgt cag ggg cag gcc aaa tta caa caa gcc gaa
     1159 378
```

```
         1161 Gly Val Gln Leu Ala Arg Gln Gly Gln Ala Lys Leu Gln Gln Ala Glu
         1162              45              50              55
E--> 1164 cag cgc gta caa att ctg ctg tct gac aat gaa gac gcc tct cta acc
         1165 426
         1167 Gln Arg Val Gln Ile Leu Leu Ser Asp Asn Glu Asp Ala Ser Leu Thr
         1168              60              65              70
E--> 1170 cct ttt aca ccg gac aat gag ta atg gac ttt ccg cag caa ctc gaa
         1171 473
W--> 1173 Pro Phe Thr Pro Asp Asn Glu    Met Asp Phe Pro Gln Gln Leu Glu
W--> 1174          75              80      1          5
E--> 1176 gcc tgc gtt aag cag gcc aac cag gcg ctg agc cgt ttt atc gcc cca
         1177 521
         1179 Ala Cys Val Lys Gln Ala Asn Gln Ala Leu Ser Arg Phe Ile Ala Pro
W--> 1180          10              15              20
E--> 1182 ctg ccc ttt cag aac act ccc gtg gtc gaa acc atg cag tat ggc gca
         1183 569
         1185 Leu Pro Phe Gln Asn Thr Pro Val Val Glu Thr Met Gln Tyr Gly Ala
W--> 1186   25              30              35              40
E--> 1188 tta tta ggt ggt aag cgc ctg cga cct ttc ctg gtt tat gcc acc ggt
         1189 617
         1191 Leu Leu Gly Gly Lys Arg Leu Arg Pro Phe Leu Val Tyr Ala Thr Gly
W--> 1192              45              50              55
E--> 1194 cat atg ttc ggc gtt agc aca aac acg ctg gac gca ccc gct gcc gcc
         1195 665
         1197 His Met Phe Gly Val Ser Thr Asn Thr Leu Asp Ala Pro Ala Ala Ala
W--> 1198          60              65              70
E--> 1200 gtt gag tgt atc cac gct tac tca tta att cat gat gat tta ccg gca
         1201 713
         1203 Val Glu Cys Ile His Ala Tyr Ser Leu Ile His Asp Asp Leu Pro Ala
W--> 1204          75              80              85
E--> 1206 atg gat gat gac gat ctg cgt cgc ggt ttg cca acc tgc cat gtg aag
         1207 761
         1209 Met Asp Asp Asp Asp Leu Arg Arg Gly Leu Pro Thr Cys His Val Lys
W--> 1210          90              95              100
E--> 1212 ttt ggc gaa gca aac gcg att ctc gct ggc gac gct tta caa acg ctg
         1213 809
         1215 Phe Gly Glu Ala Asn Ala Ile Leu Ala Gly Asp Ala Leu Gln Thr Leu
W--> 1216 105              110             115             120
E--> 1218 gcg ttc tcg att tta agc gat gcc gat atg ccg gaa gtg tcg gac cgc
         1219 857
         1221 Ala Phe Ser Ile Leu Ser Asp Ala Asp Met Pro Glu Val Ser Asp Arg
W--> 1222              125             130             135
E--> 1224 gac aga att tcg atg att tct gaa ctg gcg agc gcc agt ggt att gcc
         1225 905
         1227 Asp Arg Ile Ser Met Ile Ser Glu Leu Ala Ser Ala Ser Gly Ile Ala
W--> 1228              140             145             150
E--> 1230 gga atg tgc ggt ggt cag gca tta gat tta gac gcg gaa ggc aaa cac
         1231 953
         1233 Gly Met Cys Gly Gly Gln Ala Leu Asp Leu Asp Ala Glu Gly Lys His
```

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W--> 1234          155                   160                  165
E--> 1236 gta cct ctg gac gcg ctt gag cgt att cat cgt cat aaa acc ggc gca
     1237 1001
     1239 Val Pro Leu Asp Ala Leu Glu Arg Ile His Arg His Lys Thr Gly Ala
W--> 1240      170                   175                  180
E--> 1242 ttg att cgc gcc gcc gtt cgc ctt ggt gca tta agc gcc gga gat aaa
     1243 1049
     1245 Leu Ile Arg Ala Ala Val Arg Leu Gly Ala Leu Ser Ala Gly Asp Lys
W--> 1246 185                   190                  195                  200
E--> 1248 gga cgt cgt gct ctg ccg gta ctc gac aag tat gca gag agc atc ggc
     1249 1097
     1251 Gly Arg Arg Ala Leu Pro Val Leu Asp Lys Tyr Ala Glu Ser Ile Gly
W--> 1252              205                   210                  215
E--> 1254 ctt gcc ttc cag gtt cag gat gac atc ctg gat gtg gtg gga gat act
     1255 1145
     1257 Leu Ala Phe Gln Val Gln Asp Asp Ile Leu Asp Val Val Gly Asp Thr
W--> 1258              220                   225                  230
E--> 1260 gca acg ttg gga aaa cgc cag ggt gcc gac cag caa ctt ggt aaa agt
     1261 1193
     1263 Ala Thr Leu Gly Lys Arg Gln Gly Ala Asp Gln Gln Leu Gly Lys Ser
W--> 1264          235                   240                  245
E--> 1266 acc tac cct gca ctt ctg ggt ctt gag caa gcc cgg aag aaa gcc cgg
     1267 1241
     1269 Thr Tyr Pro Ala Leu Leu Gly Leu Glu Gln Ala Arg Lys Lys Ala Arg
W--> 1270      250                   255                  260
E--> 1272 gat ctg atc gac gat gcc cgt cag tcg ctg aaa caa ctg gct gaa cag
     1273 1289
     1275 Asp Leu Ile Asp Asp Ala Arg Gln Ser Leu Lys Gln Leu Ala Glu Gln
W--> 1276 265                   270                  275                  280
E--> 1278 tca ctc gat acc tcg gca ctg gaa gcg cta gcg gac tac atc atc cag
     1279 1337
     1281 Ser Leu Asp Thr Ser Ala Leu Glu Ala Leu Ala Asp Tyr Ile Ile Gln
W--> 1282              285                   290                  295
E--> 1284 cgt aat aaa taaacaataa gtattaatag gcccctg atg agt ttt gat att gcc
     1285 1391
     1287 Arg Asn Lys                           Met Ser Phe Asp Ile Ala
W--> 1288                                        1                   5
E--> 1290 aaa tac ccg acc ctg gca ctg gtc gac tcc acc cag gag tta cga ctg
     1291 1439
     1293 Lys Tyr Pro Thr Leu Ala Leu Val Asp Ser Thr Gln Glu Leu Arg Leu
W--> 1294              10                   15                  20
E--> 1296 ttg ccg aaa gag agt tta ccg aaa ctc tgc gac gaa ctg cgc cgc tat
     1297 1487
     1299 Leu Pro Lys Glu Ser Leu Pro Lys Leu Cys Asp Glu Leu Arg Arg Tyr
W--> 1300          25                   30                  35
E--> 1302 tta ctc gac agc gtg agc cgt tcc agc ggg cac ttc gcc tcc ggg ctg
     1303 1535
     1305 Leu Leu Asp Ser Val Ser Arg Ser Ser Gly His Phe Ala Ser Gly Leu
W--> 1306      40                   45                  50
```

```
E--> 1308 ggc acg gtc gaa ctg acc gtg gcg ctg cac tat gtc tac aac acc ccg
     1309 1583
     1311 Gly Thr Val Glu Leu Thr Val Ala Leu His Tyr Val Tyr Asn Thr Pro
W--> 1312 55                60                65                70
E--> 1314 ttt gac caa ttg att tgg gat gtg ggg cat cag gct tat ccg cat aaa
     1315 1631
     1317 Phe Asp Gln Leu Ile Trp Asp Val Gly His Gln Ala Tyr Pro His Lys
W--> 1318                  75                80                85
E--> 1320 att ttg acc gga cgc cgc gac aaa atc ggc acc atc cgt cag aaa ggc
     1321 1679
     1322 Ile Leu Thr Gly Arg Arg Asp Lys Ile Gly Thr Ile Arg Gln Lys Gly
W--> 1323             90                95                100
E--> 1325 ggt ctg cac ccg ttc ccg tgg cgc ggc gaa agc gaa tat gac gta tta
     1326 1727
     1328 Gly Leu His Pro Phe Pro Trp Arg Gly Glu Ser Glu Tyr Asp Val Leu
W--> 1329         105               110               115
E--> 1331 agc gtc ggg cat tca tca acc tcc atc agt gcc gga att ggt att gcg
     1332 1775
     1334 Ser Val Gly His Ser Ser Thr Ser Ile Ser Ala Gly Ile Gly Ile Ala
W--> 1335     120               125               130
E--> 1337 gtt gct gcc gaa aaa gaa ggc aaa aat cgc cgc acc gtc tgt gtc att
     1338 1823
     1340 Val Ala Ala Glu Lys Glu Gly Lys Asn Arg Arg Thr Val Cys Val Ile
W--> 1341 135               140               145               150
E--> 1344 ggc gat ggc gcg att acc gca ggc atg gcg ttt gaa gcg atg aat cac
     1345 1871
     1347 Gly Asp Gly Ala Ile Thr Ala Gly Met Ala Phe Glu Ala Met Asn His
W--> 1348               155               160               165
E--> 1350 gcg ggc gat atc cgt cct gat atg ctg gtg att ctc aac gac aat gaa
     1351 1919
     1353 Ala Gly Asp Ile Arg Pro Asp Met Leu Val Ile Leu Asn Asp Asn Glu
W--> 1354               170               175               180
E--> 1356 atg tcg att tcc gaa aat gtc ggc gcg ctc aac aac cat ctg gca cag
     1357 1967
     1359 Met Ser Ile Ser Glu Asn Val Gly Ala Leu Asn Asn His Leu Ala Gln
W--> 1360         185               190               195
E--> 1362 ctg ctt tcc ggt aag ctt tac tct tca ctg cgc gaa ggc ggg aaa aaa
     1363 2015
     1365 Leu Leu Ser Gly Lys Leu Tyr Ser Ser Leu Arg Glu Gly Gly Lys Lys
W--> 1366     200               205               210
E--> 1368 gtt ttc tct ggc gtg ccg cca att aaa gag ctg ctc aaa cgc acc gaa
     1369 2063
     1371 Val Phe Ser Gly Val Pro Pro Ile Lys Glu Leu Leu Lys Arg Thr Glu
W--> 1372 215               220               225               230
E--> 1374 gaa cat att aaa ggc atg gta gtg cct ggc acg ttg ttt gaa gag ctg
     1375 2111
     1377 Glu His Ile Lys Gly Met Val Val Pro Gly Thr Leu Phe Glu Glu Leu
W--> 1378               235               240               245
E--> 1380 ggc ttt aac tac atc ggc ccg gtg gac ggt cac gat gtg ctg ggg ctt
```

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        1381 2159
        1383 Gly Phe Asn Tyr Ile Gly Pro Val Asp Gly His Asp Val Leu Gly Leu
W--> 1384             250             255             260
E--> 1386 atc acc acg cta aag aac atg cgc gac ctg aaa ggc ccg cag ttc ctg
        1387 2207
        1389 Ile Thr Thr Leu Lys Asn Met Arg Asp Leu Lys Gly Pro Gln Phe Leu
W--> 1390             265             270             275
E--> 1392 cat atc atg acc aaa aaa ggt cgt ggt tat gaa ccg gca gaa aaa gac
        1393 2255
        1395 His Ile Met Thr Lys Lys Gly Arg Gly Tyr Glu Pro Ala Glu Lys Asp
W--> 1396         280             285             290
E--> 1398 ccg atc act ttc cac gcc gtg cct aaa ttt gat ccc tcc agc ggt tgt
        1399 2303
        1401 Pro Ile Thr Phe His Ala Val Pro Lys Phe Asp Pro Ser Ser Gly Cys
W--> 1402 295             300             305             310
E--> 1404 ttg ccg aaa agt agc ggc ggt ttg ccg agc tat tca aaa atc ttt ggc
        1405 2351
        1407 Leu Pro Lys Ser Ser Gly Gly Leu Pro Ser Tyr Ser Lys Ile Phe Gly
W--> 1408             315             320             325
E--> 1410 gac tgg ttg tgc gaa acg gca gcg aaa gac aac aag ctg atg gcg att
        1411 2399
        1413 Asp Trp Leu Cys Glu Thr Ala Ala Lys Asp Asn Lys Leu Met Ala Ile
W--> 1414             330             335             340
E--> 1416 act ccg gcg atg cgt gaa ggt tcc ggc atg gtc gag ttt tca cgt aaa
        1417 2447
        1419 Thr Pro Ala Met Arg Glu Gly Ser Gly Met Val Glu Phe Ser Arg Lys
W--> 1420             345             350             355
E--> 1422 ttc ccg gat cgc tac ttc gac gtg gca att gcc gag caa cac gcg gtg
        1423 2495
        1425 Phe Pro Asp Arg Tyr Phe Asp Val Ala Ile Ala Glu Gln His Ala Val
W--> 1426         360             365             370
E--> 1428 acc ttt gct gcg ggt ctg gcg att ggt ggg tac aaa ccc att gtc gcg
        1429 2543
        1431 Thr Phe Ala Ala Gly Leu Ala Ile Gly Gly Tyr Lys Pro Ile Val Ala
W--> 1432 375             380             385             390
E--> 1434 att tac tcc act ttc ctg caa cgc gcc tat gat cag gtg ctg cat gac
        1435 2591
        1437 Ile Tyr Ser Thr Phe Leu Gln Arg Ala Tyr Asp Gln Val Leu His Asp
W--> 1438             395             400             405
E--> 1440 gtg gcg att caa aag ctt ccg gtc ctg ttc gcc atc gac cgc gcg ggc
        1441 2639
        1443 Val Ala Ile Gln Lys Leu Pro Val Leu Phe Ala Ile Asp Arg Ala Gly
W--> 1444             410             415             420
E--> 1446 att gtt ggt gct gac ggt caa acc cat cag ggt gct ttt gat ctc tct
        1447 2687
        1449 Ile Val Gly Ala Asp Gly Gln Thr His Gln Gly Ala Phe Asp Leu Ser
W--> 1450             425             430             435
E--> 1452 tac ctg cgc tgc ata ccg gaa atg gtc att atg acc ccg agc gat gaa
        1453 2735
```

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```
        1455 Tyr Leu Arg Cys Ile Pro Glu Met Val Ile Met Thr Pro Ser Asp Glu
W--> 1456     440             445             450
E--> 1458 aac gaa tgt cgc cag atg ctc tat acc ggc tat cac tat aac gat ggc
     1459 2783
        1461 Asn Glu Cys Arg Gln Met Leu Tyr Thr Gly Tyr His Tyr Asn Asp Gly
W--> 1462 455             460             465             470
E--> 1464 ccg tca gcg gtg cgc tac ccg cgt ggc aac gcg gtc ggc gtg gaa ctg
     1465 2831
        1467 Pro Ser Ala Val Arg Tyr Pro Arg Gly Asn Ala Val Gly Val Glu Leu
W--> 1468             475             480             485
E--> 1470 acg ccg ctg gaa aaa cta cca att ggc aaa ggc att gtg aag cgt cgt
     1471 2879
        1473 Thr Pro Leu Glu Lys Leu Pro Ile Gly Lys Gly Ile Val Lys Arg Arg
W--> 1474             490             495             500
E--> 1476 ggc gag aaa ctg gcg atc ctt aac ttt ggt acg ctg atg cca gaa gcg
     1477 2927
        1479 Gly Glu Lys Leu Ala Ile Leu Asn Phe Gly Thr Leu Met Pro Glu Ala
W--> 1480     505             510             515
E--> 1482 gcg aaa gtc gcc gaa tcg ctg aac gcc acg ctg gtc gat atg cgt ttt
     1483 2975
        1485 Ala Lys Val Ala Glu Ser Leu Asn Ala Thr Leu Val Asp Met Arg Phe
W--> 1486     520             525             530
E--> 1488 gtg aaa ccg ctt gat gaa gcg tta att ctg gaa atg gcc gcc agc cat
     1489 3023
        1491 Val Lys Pro Leu Asp Glu Ala Leu Ile Leu Glu Met Ala Ala Ser His
W--> 1492 535             540             545             550
E--> 1494 gaa gcg ctg gtc acc gta gaa gaa aac gcc att atg ggc ggc gca ggc
     1495 3071
        1497 Glu Ala Leu Val Thr Val Glu Glu Asn Ala Ile Met Gly Gly Ala Gly
W--> 1498             555             560             565
E--> 1500 agc ggc gtg aac gaa gtg ctg atg gcc cat cgt aaa cca gta ccc gtg
     1501 3119
        1503 Ser Gly Val Asn Glu Val Leu Met Ala His Arg Lys Pro Val Pro Val
W--> 1504             570             575             580
E--> 1506 ctg aac att ggc ctg ccg gac ttc ttt att ccg caa gga act cag gaa
     1507 3167
        1509 Leu Asn Ile Gly Leu Pro Asp Phe Phe Ile Pro Gln Gly Thr Gln Glu
W--> 1510     585             590             595
E--> 1512 gaa atg cgc gcc gaa ctc ggc ctc gat gcc gct ggt atg gaa gcc aaa
     1513 3215
        1515 Glu Met Arg Ala Glu Leu Gly Leu Asp Ala Ala Gly Met Glu Ala Lys
W--> 1516     600             605             610
E--> 1518 atc aag gcc tgg ctg gca taatccctac tccactcctg ctatgcttaa
     1519 3263
        1521 Ile Lys Ala Trp Leu Ala
W--> 1522 615             620
E--> 1524 gaaattattc atagactcta aataattcga gttgcaggaa ggcggcaaac gagtgaagcc
     1525 3323
E--> 1528 ccaggagctt acataagtaa gtg act ggg gtg aac gaa tgc agc cgc agc aca
```

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            Input Set : A:\1241.16 sequence.txt
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        1529 3376
        1531                   Val Thr Gly Val Asn Glu Cys Ser Arg Ser Thr
W--> 1532                       1               5                  10
E--> 1534 tgc aac ttg aag tat gac gag tat agc agg agt ggc agc atg caa tac
        1535 3424
        1537 Cys Asn Leu Lys Tyr Asp Glu Tyr Ser Arg Ser Gly Ser Met Gln Tyr
W--> 1538            15              20                  25
E--> 1540 aac ccc tta gga aaa acc gac ctt cgc gtt tcc cga ctt tgc ctc ggc
        1541 3472
        1543 Asn Pro Leu Gly Lys Thr Asp Leu Arg Val Ser Arg Leu Cys Leu Gly
W--> 1544            30              35                  40
E--> 1546 tgt atg acc ttt ggc gag cca gat cgc ggt aat cac gca tgg aca ctg
        1547 3520
        1549 Cys Met Thr Phe Gly Glu Pro Asp Arg Gly Asn His Ala Trp Thr Leu
W--> 1550        45              50                  55
E--> 1552 ccg gaa gaa agc agc cgt ccc ata att aaa cgt gca ctg gaa ggc ggc
        1553 3568
        1555 Pro Glu Glu Ser Ser Arg Pro Ile Ile Lys Arg Ala Leu Glu Gly Gly
W--> 1556    60              65                  70                  75
E--> 1558 ata aat ttc ttt gat acc gcc aac agt tat tct gac ggc agc agc gaa
        1559 3616
        1561 Ile Asn Phe Phe Asp Thr Ala Asn Ser Tyr Ser Asp Gly Ser Ser Glu
W--> 1562            80              85                  90
E--> 1564 gag atc gtc ggt cgc gca ctg cgg gat ttc gcc cgt cgt gaa gac gtg
        1565 3664
        1567 Glu Ile Val Gly Arg Ala Leu Arg Asp Phe Ala Arg Arg Glu Asp Val
W--> 1568            95              100                 105
E--> 1570 gtc gtt gcg acc aaa gtg ttc cat cgc gtt ggt gat tta ccg gaa gga
        1571 3712
        1573 Val Val Ala Thr Lys Val Phe His Arg Val Gly Asp Leu Pro Glu Gly
W--> 1574            110             115                 120
E--> 1575 tta tcc cgt gcg caa att ttg cgc tct atc gac gac agc ctg cga cgt
        1576 3760
        1578 Leu Ser Arg Ala Gln Ile Leu Arg Ser Ile Asp Asp Ser Leu Arg Arg
W--> 1579        125             130                 135
E--> 1581 ctc ggc atg gat tat gtc gat atc ctg caa att cat cgc tgg gat tac
        1582 3808
        1584 Leu Gly Met Asp Tyr Val Asp Ile Leu Gln Ile His Arg Trp Asp Tyr
W--> 1585 140             145                 150                 155
E--> 1587 aac acg ccg atc gaa gag acg ctg gaa gcc ctc aac gac gtg gta aaa
        1588 3856
        1590 Asn Thr Pro Ile Glu Glu Thr Leu Glu Ala Leu Asn Asp Val Val Lys
W--> 1591            160             165                 170
E--> 1593 gcc ggg aaa gcg cgt tat atc ggc gcg tca tca atg cac gct tcg cag
        1594 3904
        1596 Ala Gly Lys Ala Arg Tyr Ile Gly Ala Ser Ser Met His Ala Ser Gln
W--> 1597            175             180                 185
E--> 1599 ttt gct cag gca ctg gaa ctc caa aaa cag cac ggc tgg gcg cag ttt
        1600 3952
```

same

```
                    Input Set : A:\1241.16 sequence.txt
                    Output Set: N:\CRF3\12262000\I673198.raw


        1602 Phe Ala Gln Ala Leu Glu Leu Gln Lys Gln His Gly Trp Ala Gln Phe
W--> 1603          190             195             200
E--> 1605 gtc agt atg cag gat cac tac aat ctg att tat cgt gaa gaa gag cgc
        1606 4000
        1608 Val Ser Met Gln Asp His Tyr Asn Leu Ile Tyr Arg Glu Glu Glu Arg
W--> 1609     205             210             215
E--> 1611 gag atg cta cca ctg tgt tat cag gag ggc gtg gcg gta att cca tgg
        1612 4048
        1614 Glu Met Leu Pro Leu Cys Tyr Gln Glu Gly Val Ala Val Ile Pro Trp
W--> 1615 220             225             230             235
E--> 1617 agc ccg ctg gca agg ggc cgt ctg acg cgt ccg tgg gga gaa act acc
        1618 4096
        1620 Ser Pro Leu Ala Arg Gly Arg Leu Thr Arg Pro Trp Gly Glu Thr Thr
W--> 1621             240             245             250
E--> 1623 gca cga ctg gtg tct gat gag gtg ggg aaa aat ctc tat aaa gaa agc
        1624 4144
        1626 Ala Arg Leu Val Ser Asp Glu Val Gly Lys Asn Leu Tyr Lys Glu Ser
W--> 1627         255             260             265
E--> 1629 gat gaa aat gac gcg cag atc gca gag cgg tta aca ggc gtc agt gaa
        1630 4192
        1632 Asp Glu Asn Asp Ala Gln Ile Ala Glu Arg Leu Thr Gly Val Ser Glu
W--> 1633         270             275             280
E--> 1635 gaa ctg ggg gcg aca cga gca caa gtt gcg ctg gcc tgg ttg ttg agt
        1636 4240
        1638 Glu Leu Gly Ala Thr Arg Ala Gln Val Ala Leu Ala Trp Leu Leu Ser
W--> 1639         285             290             295
E--> 1641 aaa ccg ggc att gcc gca ccg att atc gga act tcg cgc gaa gaa cag
        1642 4288
        1644 Lys Pro Gly Ile Ala Ala Pro Ile Ile Gly Thr Ser Arg Glu Glu Gln
W--> 1645 300             305             310             315
E--> 1647 ctt gat gag cta ttg aac gcg gtg gat atc act ttg aag ccg gaa cag
        1648 4336
        1650 Leu Asp Glu Leu Leu Asn Ala Val Asp Ile Thr Leu Lys Pro Glu Gln
W--> 1651             320             325             330
E--> 1653 att gcc gaa ctg gaa acg ccg tat aaa ccg cat cct gtc gta gga ttt
        1654 4384
        1656 Ile Ala Glu Leu Glu Thr Pro Tyr Lys Pro His Pro Val Val Gly Phe
W--> 1657             335             340             345
E--> 1659 aaa taa
        1660 4390
        1662 Lys
        1665 <210> SEQ ID NO: 12
        1666 <211> LENGTH: 33
        1667 <212> TYPE: DNA
        1668 <213> ORGANISM: Artificial Sequence
        1670 <220> FEATURE:
        1671 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA
        1673 <400> SEQUENCE: 12
E--> 1674 ccggatccat ggcggcaatg gttcgttggc aag
```
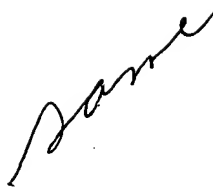
RAW SEQUENCE LISTING   DATE: 12/26/2000
PATENT APPLICATION: US/09/673,198   TIME: 13:19:35

Input Set : A:\1241.16 sequence.txt
Output Set: N:\CRF3\12262000\I673198.raw

```
      1675 33
      1679 <210> SEQ ID NO: 13
      1680 <211> LENGTH: 34
      1681 <212> TYPE: DNA
      1682 <213> ORGANISM: Artificial Sequence
      1684 <220> FEATURE:
      1685 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA
      1687 <400> SEQUENCE: 13
E--> 1688 ccgaattctt atttaaatcc tacgacagga tgcg
      1689 34
      1693 <210> SEQ ID NO: 14
      1694 <211> LENGTH: 33
      1695 <212> TYPE: DNA
      1696 <213> ORGANISM: Artificial Sequence
      1698 <220> FEATURE:
      1699 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA
      1701 <400> SEQUENCE: 14
E--> 1702 ccggatccat gagttttgat attgccaaat acc
      1703 33
      1707 <210> SEQ ID NO: 15
      1708 <211> LENGTH: 33
      1709 <212> TYPE: DNA
      1710 <213> ORGANISM: Artificial Sequence
      1712 <220> FEATURE:
      1713 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA
      1715 <400> SEQUENCE: 15
E--> 1716 ccgaattctt atgccagcca ggccttgatt ttg
      1717 33
      1721 <210> SEQ ID NO: 16
      1722 <211> LENGTH: 33
      1723 <212> TYPE: DNA
      1724 <213> ORGANISM: Artificial Sequence
      1726 <220> FEATURE:
      1727 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA
      1729 <400> SEQUENCE: 16
E--> 1730 ccgaattctt actcattgtc cggtgtaaaa ggg
      1731 33
      1735 <210> SEQ ID NO: 17
      1736 <211> LENGTH: 33
      1737 <212> TYPE: DNA
      1738 <213> ORGANISM: Artificial Sequence
      1740 <220> FEATURE:
      1741 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA
      1743 <400> SEQUENCE: 17
E--> 1744 ccggatccat ggactttccg cagcaactcg aag
      1745 33
      1749 <210> SEQ ID NO: 18
      1750 <211> LENGTH: 33
      1751 <212> TYPE: DNA
```

```
                 RAW SEQUENCE LISTING              DATE: 12/26/2000
                 PATENT APPLICATION:  US/09/673,198   TIME: 13:19:35

                 Input Set : A:\1241.16 sequence.txt
                 Output Set: N:\CRF3\12262000\I673198.raw

       1752 <213> ORGANISM: Artificial Sequence
       1754 <220> FEATURE:
       1755 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA
       1757 <400> SEQUENCE: 18
E-->   1758 ccgaattctt atttattacg ctggatgatg tag
       1759 33
       1763 <210> SEQ ID NO: 19
       1764 <211> LENGTH: 33
       1765 <212> TYPE: DNA
       1766 <213> ORGANISM: Artificial Sequence
       1768 <220> FEATURE:
       1769 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA
       1771 <400> SEQUENCE: 19
E-->   1772 ccggatccta atccctactc cactcctgct atg
       1773 33
       1777 <210> SEQ ID NO: 20
       1778 <211> LENGTH: 30
       1779 <212> TYPE: DNA
       1780 <213> ORGANISM: Artificial Sequence
       1782 <220> FEATURE:
       1783 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA
       1785 <400> SEQUENCE: 20
E-->   1786 gggggatcca agcaactcac cattctgggc
       1787 30
       1791 <210> SEQ ID NO: 21
       1792 <211> LENGTH: 30
       1793 <212> TYPE: DNA
       1794 <213> ORGANISM: Artificial Sequence
       1796 <220> FEATURE:
       1797 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA
       1799 <400> SEQUENCE: 21
E-->   1800 gggggatccg cttgcgagac gcatcacctc
       1801 30
       1805 <210> SEQ ID NO: 22
       1806 <211> LENGTH: 32
       1807 <212> TYPE: DNA
       1808 <213> ORGANISM: Artificial Sequence
       1810 <220> FEATURE:
       1811 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA
       1813 <400> SEQUENCE: 22
E-->   1814 gggggatcca gttttgatat tyccaaatac cc
       1815 32
       1819 <210> SEQ ID NO: 23
       1820 <211> LENGTH: 32
       1821 <212> TYPE: DNA
       1822 <213> ORGANISM: Artificial Sequence
       1824 <220> FEATURE:
       1825 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA
       1827 <400> SEQUENCE: 23
```

RAW SEQUENCE LISTING   DATE: 12/26/2000
PATENT APPLICATION: US/09/673,198   TIME: 13:19:35

Input Set : A:\1241.16 sequence.txt
Output Set: N:\CRF3\12262000\I673198.raw

```
E--> 1828 gggggatcct gccagccagg ccttgatttt gg
     1829 32
     1833 <210> SEQ ID NO: 24
     1834 <211> LENGTH: 30
     1835 <212> TYPE: DNA
     1836 <213> ORGANISM: Artificial Sequence
     1838 <220> FEATURE:
     1839 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA
     1841 <400> SEQUENCE: 24
E--> 1842 gggggatccg agcaactcac cattctgggc
     1843 30
     1847 <210> SEQ ID NO: 25
     1848 <211> LENGTH: 30
     1849 <212> TYPE: DNA
     1850 <213> ORGANISM: Artificial Sequence
     1852 <220> FEATURE:
     1853 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA
     1855 <400> SEQUENCE: 25
E--> 1856 gggggatccg cttgcgagac gcatcacctc
     1857 30
```

```
VERIFICATION SUMMARY                    DATE: 12/26/2000
PATENT APPLICATION:  US/09/673,198      TIME: 13:19:36

Input Set : A:\1241.16 sequence.txt
Output Set: N:\CRF3\12262000\I673198.raw
```

```
L:9 M:201 W: Mandatory field data missing. FILE REFERENCE
L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:402 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:48 SEQ:6
M:254 Repeated in SeqNo=6
L:647 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:48 SEQ:7
M:254 Repeated in SeqNo=7
L:772 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:48 SEQ:8
M:254 Repeated in SeqNo=8
L:813 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:48 SEQ:9
M:254 Repeated in SeqNo=9
L:956 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:48 SEQ:10
M:254 Repeated in SeqNo=10
L:1128 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:11
M:254 Repeated in SeqNo=11
L:1173 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:1174 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1180 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1186 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1192 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1198 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1204 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1210 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1216 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1222 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1228 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1234 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1240 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1246 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1252 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1258 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1264 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1270 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1276 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1282 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1288 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1294 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1300 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1306 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1312 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1318 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1323 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1329 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1335 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1341 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1348 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1354 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1360 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
```

VERIFICATION SUMMARY   DATE: 12/26/2000
PATENT APPLICATION: US/09/673,198 TIME: 13:19:36

Input Set : A:\1241.16 sequence.txt
Output Set: N:\CRF3\12262000\I673198.raw

```
L:1366 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1372 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1378 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1384 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1390 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1396 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1402 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1408 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1414 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1420 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1426 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1432 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1438 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1444 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1450 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1456 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1462 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1468 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1674 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:33 SEQ:12
L:1688 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:34 SEQ:13
L:1702 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:33 SEQ:14
L:1716 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:33 SEQ:15
L:1730 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:33 SEQ:16
L:1744 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:33 SEQ:17
L:1758 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:33 SEQ:18
L:1772 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:33 SEQ:19
L:1786 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:30 SEQ:20
L:1800 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:30 SEQ:21
L:1814 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:32 SEQ:22
L:1828 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:32 SEQ:23
L:1842 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:30 SEQ:24
L:1856 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:30 SEQ:25
L:1997 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:48 SEQ:27
M:254 Repeated in SeqNo=27
L:2338 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:48 SEQ:29
M:254 Repeated in SeqNo=29
L:2636 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:48 SEQ:31
M:254 Repeated in SeqNo=31
L:2771 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:23 SEQ:32
L:2784 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:23 SEQ:33
L:2797 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:23 SEQ:34
```